

In such a case, one would return to the lab and obtain additional information to resolve the ambiguity. The multi-alignment, or consensus, phase uses more information than just the pairwise alignments in the layout. The sequences of all the fragments in a layout are simultaneously aligned, giving a final set of contigs representing regions of the target genome. An example of an assembly program is PHRAP, which can be found on the world wide web at [chimera.biotech.washington.edu/UWGC/tools/phrap.htm](http://chimera.biotech.washington.edu/UWGC/tools/phrap.htm).

***In the Claims:***

Please enter the following amended claims:

1. (Twice Amended) A substantially purified nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 or the complement thereof.

17. (Twice Amended) A substantially purified nucleic acid molecule having between 90% and 100% sequence identity with a nucleic acid molecule having the sequence of SEQ ID NO: 1 or complements thereof.

18. (Once Amended) The substantially purified nucleic acid molecule of claim 17, wherein said substantially purified nucleic molecule has between 99% and 100% sequence identity with a nucleic acid molecule having the sequence of SEQ ID NO: 1 or complements thereof.

***Remarks***

Following entry of this amendment, claims 1-4, 6-9, and 16-20 will be pending. Claims 1, 17 and 18 have been amended. Support for the claims may be found throughout the specification. No new matter is added by these amendments.